

```

seq_documentation_block:
LOCUS      AF114024      357 bp      mRNA           INV      27-JAN-2000
DEFINITION Buthus martensii neurotoxin P01 (P01) mRNA, complete cds.
ACCESSION  AF114024
VERSION    AF114024.1  GI:6690265
KEYWORDS   .
SOURCE     Chinese scorpion.
ORGANISM   Buthus martensii
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.
REFERENCE  1 (bases 1 to 357)
AUTHORS   Zhu,S.-Y., Zeng,X.-C., Li,W.-X. and Jiang,D.-H.
TITLE     Molecular characterization of a K+ channel blocker from Buthus
martensii
JOURNAL   Chin. Sci. Bull. 44 (21), 2295-2299 (1999)
REFERENCE  2 (bases 1 to 357)
AUTHORS   Zhu,S.-Y., Zeng,X.-C., Li,W.-X. and Jiang,D.-H.
TITLE     Direct Submission
JOURNAL   Submitted (14-DEC-1998) Virology, Life Science, Luojia Mountain,
Wuhan, Hubei 430072, China
FEATURES  source          Location/Qualifiers
          1. .357
          /organism="Buthus martensii"
          /db_xref="taxon:34649"
          /tissue_type="venom gland"
          /note="synonym: Mesobuthus martensii; authority: Buthus
          martensii Karsch"
gene       1. .357
          /gene="P01"
          68. .241
          /gene="P01"
          /function="potassium ion channel blocker"
          /codon_start=1
          /product="neurotoxin P01"
          /protein_id="AAF24057.1"
          /db_xref="GI:6690266"
          /translation="MSRLYAIILIALVFNVIMTIIPDMKVEATCEDCPEHCATQNAR
AKCDNDKCVCEPK"
CDS        BASE COUNT      156 a      68 c      60 g      73 t
ORIGIN

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alignment_scores:
Quality: 110.00          Length:      57
Ratio: 2.444              Gaps:         3
Percent Similarity: 78.947 Percent Identity: 43.860

```

```

alignment_block:
US-09-599-416-2 x AF114024 ..
```

```
Align seg 1/1 to: AF114024 from: 1 to: 357
```

```

1 MetSerArgIlePheThrIleIleLeuIleValPheAlaLeuAsnIleIle 17
|||||||||:::||||||:||||||:||||||:||||||:||||||:|||:::|||
68 ATGAGTCGACTTATGCAATCATCTTAATTGCTCTTGCTCAATGTGAT 117

```

17 eIleSer...LeuSerAsnPheLysValGluAlaAlaGlnCysTyrSers 33
|::::::::::: :::: ::::::::::||||||||||| ||| :
118 TATGACGATTATAACCGATATGAAAGTAGAGGCTGCTACCTGT.....G 161

33 erAspCysArgValLysCysAlaAlaMetGlyPheAsnSerGlyLysCys 49
:::|||||| |||||||:|||||: ::::::: ::::::: |||||||
162 AAGATTGCCCGAGCACTGTGCCACACAGAATGCCGAGCA...AAATGC 208

50 IleAsnSerLysCysLysCys 56
|||:|||:||| |||
209 GATAATGACAAATGCGTATGT 229